1A. MOUSE AIOLOS cDNA SEQUENCE

CACGAGCGCACACCGCTCGGCTCTCCTTGCGACACGCCCTCATCCCCGGTGTT
TCTCAAGTAGACGTCCCGAGACGGTCGCTGAGGCACTGTTTCCACGCGATCA
GGGTTCCTCAGGCTTGACATTCAAAAGTGGGTGCGGAACCCGCGGCACTCGG
AGCGTGCTTTAAAGCGGCCGCCAGCCAGCGCCGCTCTAACCTCGCGCCCCGG
CTGCCGGCGGCTCCCGCCCTGCATCTGCGCCGACGCGACCGAGCGATCCCGG
GGCCTCCCTGCGCCCGGAATCTCCCGCCAGCCGCGCGGGTCCCCACGGCAGC
AGCACGTGGAGCGGCCGCGGAGCCTGAGCGACAGCTGCAGCCCGCGCGGCC
CGCGGCGACATGGAAGATATACAACCGACTGTGGAGCTGAAAAGCACGGAG
GAGCAGCCTCTGCCCACAGAGAGCCCAGACGCTCTGAATGACTACAGCTTGC
CCAAACCTCATGAGATAGAAAACGTGGACAGTAGAGAAGCCCCAGCCAATG
AAGACGAAGATGCAGGAGAAGATTCGATGAAAGTGAAAGATGAATACAGCG
ACAGAGATGAGAACATTATGAAGCCGGAGCCCATGGGAGATGCAGAAGAGA
GTGAAATGCCTTACAGCTATGCAAGAGAATACAGCGACTATGAAAGCATTAA
GCTGGAGAGACACGTGCCCTATGACAACAGCAGACCAACCAGTGGGAAGAT
GAACTGCGACGTGTGCGGGTTATCCTGCATTAGCTTCAACGTCTTGATGGTTC
ATAAGCGAAGCCATACCGGCGAACGCCCGTTCCAGTGTAATCAGTGCGGGGC
ATCTTTTACTCAGAAAGGTAACCTCCTCCGTCATATTAAACTGCACACGGGGG
AAAAACCTTTTAAGTGTCACCTCTGCAACTACGCATGCCAAAGGAGAGATGC
GCTCACGGGACACCTTAGGACACATTCTGTGGAGAAGCCGTACAAGTGTGAG
TTCTGCGGAAGAAGCTACAAGCAGAGAAGCTCCCTGGAGGAGCACAAGGAA
CGCTGCCGAGCTTTTCTTCAGAACCCTGACCTGGGGGACGCTGCAAGTGTGG
AGGCAAGACACATCAAAGCCGAGATGGGAAGTGAGAGAGCTCTCGTCCTGG
ACAGATTAGCAAGCAATGTGGCTAAGCGAAAAAGCTCGATGCCTCAGAAATT
CATCGGTGAGAAGCGGCACTGCTTCGATGCCAACTACAATCCCGGCTACATG
TACGAGAAGGAGAACGAGATGATGCAGACCCGGATGATGGACCAAGCCATC
AATAACGCCATCAGCTATCTAGGGGCTGAAGCCTTCCGCCCCTTAGTCCAGA
CTCCGCCTGCTCCCACCTCTGAGATGGTCCCAGTCATCAGCAGTGTGTACCCC
ATAGCACTTACTCGGGCCGATATGCCAATGGGGGCCCCGCAgGAGATGGAAA
AGAAACGGATCCTCCTGCCAGAGAAGATCTTGCCTTCTGAACGAGGTCTGTC
CCCCAATAACAGTGCCCAGGACTCCACAGACACCGACAGCAACCACGAGGAT
CGCCAACATCTCTACCAGCAAAGCCACGTGGTCCTCCCCCAGGCCCGCAATG
GGATGCCTCTTCTGAAGGAGGTCCCTCGCTCTTTTGAACTCCTCAAGCCCCCT
CCCATCTGCCTGAGGGACTCCATCAAAGTGATCAACAAAGAAGGGGAGGTGA
TGGATGTGTTTCGATGTGACCACTGCCACGTCCTCTTCCTAGATTATGTGATG
TTCACCATCCACATGGGGTGCCATGGTTTCCGTGATCCCTTTGAGTGTAACAT
GTGTGGCTATCGAAGCCACGATCGCTATGAGTTCTCCTCTCACATCGCCAGAG
GAGAGCACAGAGCCATGTTGAAGTGAGCATCTGTCCTCAATGCGAGGGTCAA
CATTGTTTTTTAAAGCTGATGGTAGCCTTATCCAGTAGACTGAACTCAAACCC
ACCTCGAG

FIG. 1A

1B. MOUSE AIOLOS PEPTIDE SEQUENCE

MEDIQPTVELKSTEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGED
SMKVKDEYSDRDENIMKPEPMGDAEESEMPYSYAREYSDYESIKLERHVPYDNS
RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHI
KLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEE
HKERCRAFLQNPDLGDAASVEARHIKAEMGSERALVLDRLASNVAKRKSSMPQ
KFIGEKRHCFDANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQ
TPPAPTSEMVPVISSVYPIALTRADMPMGAPQEMEKKRILLPEKILPSERGLSPNN
SAQDSTDTDSNHEDRQHLYQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRD
SIKVINKEGEVMDVFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCGYRSH
DRYEFSSHIARGEHRAMLK

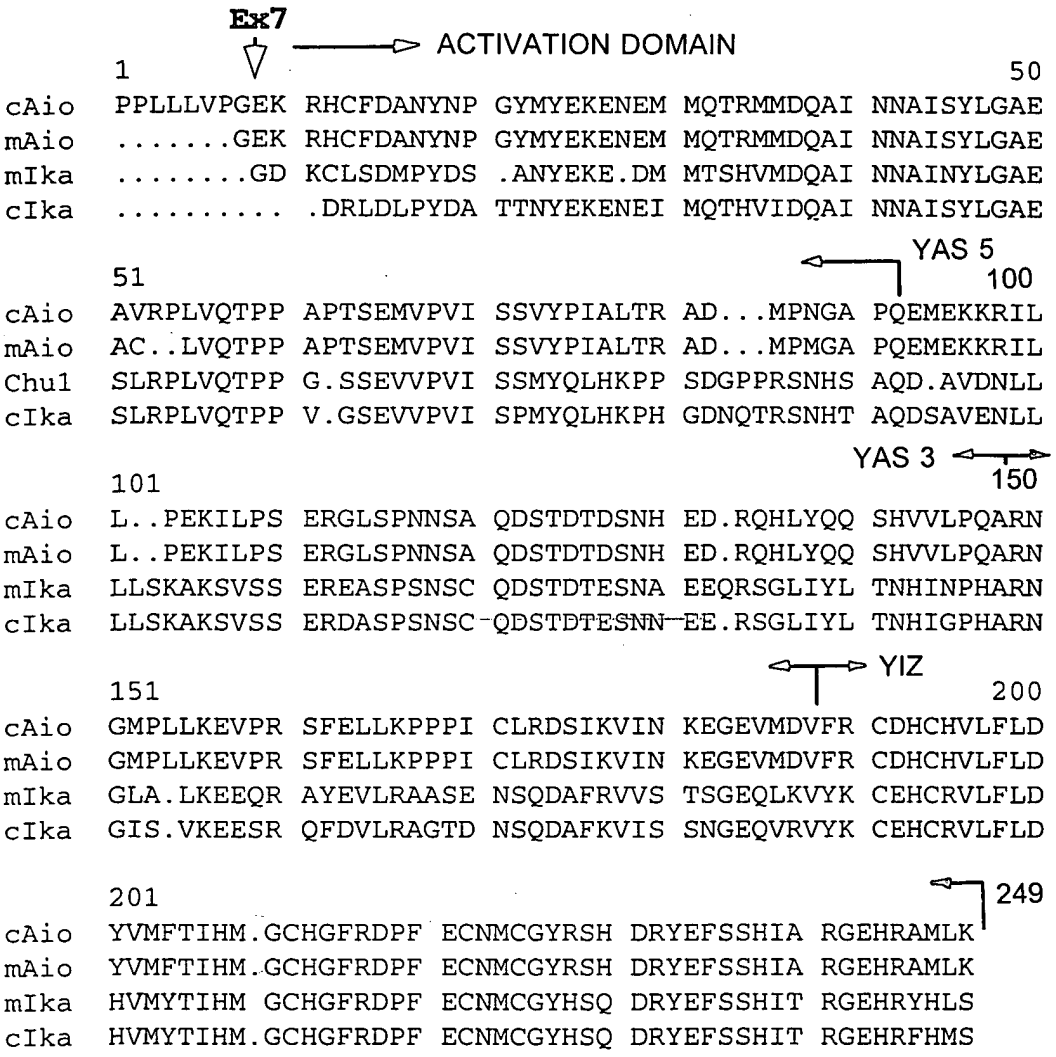
FIG. 1B

```
     1                                                    50
 aio ..........  ..........  ..........  ..........  ..........
Ik1  MDVDEGQDMS QVSGKESPPV SDTPDEGDEP MPVPEDLSTT SGAQQNSKSD

     51                                                   100
 aio ..........  ..........  ..........  ..........  ..........
Ik1  RGMASNVKVE TQSDEENGRA CEMNGEECAE DLRMLDASGE KMNGSHRDQG
                                                    Ex4
     101                                                  150
 Ik  ..........  NSARGKMNCD VCGLSCISFN VLMVHKRTHT GERPFQCNQC
Ik1  SSALSGVGGI RLPNGKLKCD ICGIVCIGPN VLMVHKRSHT GERPFQCNQC
                                                        Ex5
     151                                                  200
 aio GASFTQKGNL LRHIKLHTGE KPFKCHLCNY ACQRRDALTG HLRTHSVEKP
Ik1  GASFTQKGNL LRHIKLHSGE KPFKCHLCNY ACRRRDALTG HLRTHSVGKP
                                                Ex6
     201                                                  250
 Aio YKCEFCGRSY KQRSSLEEHK ERCRAFLQNP DLGDAASV.. ......EARH
Ik1  HKCGYCGRSY KQRSSLEEHK ERCHNYLESM GLPGMYPVIK EETNHNEMAE
                                            Ex7
     251                                                  300
 Aio IKAEMGSERA LVLDRLASNV AKRKSSMPQK FIGEKRHCFD ANYNPGYMYE
Ik1  DLCKIGAERS LVLDRLASNV AKRKSSMPQK FLGDK..CLS DMPYDSANYE

     301                                                  350
 Aio KENEMMQTRM MDQ.......  ..........  ..........  ..........
Ik1  KE.DMMTSHV MDQ
```

FIG. 3



YAS 5 = interaction domain

YAS 3 = interaction domain

YIZ = Ikaros dimerization domain

FIG. 2

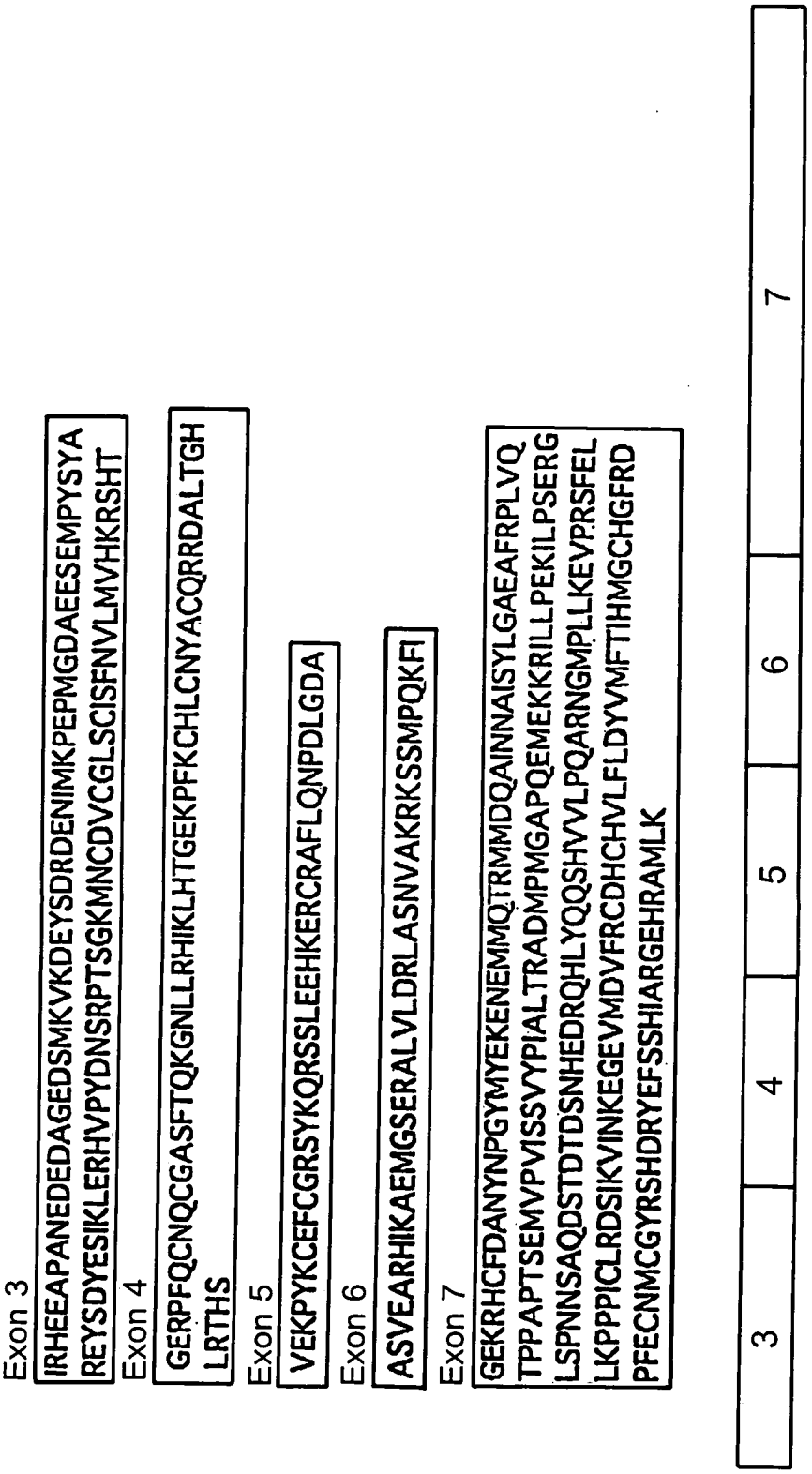


FIG. 4

FIG. 5A

Lipman-Pearson Protein Alignment
kTuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>209) human Aiolos protein AioC/hAio2	Seq2(1>508) mouseaiolos.protein	Similarity Index	Gap Length	Gap Number	Concensus Length
(1>209)	(66>273)	89.5	1	1	209

```
human Aiolos protein AioC/hAio2  ERDENVLKSEPMGNAEEPEIPYSYSREYNEYENIKLERHVVSFDSSRPTSGKMNCDVCGL  60
                                 : RDEN: : K: EPMG: AEE: E: PYSY: REY: : YE: IKLERHV : : D: SRPTSGKMNCDVCGL
mouseaiolos.protein              DRDENIMKPEPMGDAEESEMPYSYAREYSDYESIKLERHV-PYDNSRPTSGKMNCDVCGL  124

human Aiolos protein AioC/hAio2  SCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQR  120
                                 SCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQR
mouseaiolos.protein              SCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQR  184

human Aiolos protein AioC/hAio2  RDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQSTDPGDTASAEARHIK  180
                                 RDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCR: FLQ: . D GD: AS. EARHIK
mouseaiolos.protein              RDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNPDLGDAASVEARHIK  244

human Aiolos protein AioC/hAio2  AEMGSERALVLDRLASNVAKRKSSMPQKF  209
                                 AEMGSERALVLDRLASNVAKRKSSMPQKF
mouseaiolos.protein              AEMGSERALVLDRLASNVAKRKSSMPQKF  273
```

FIG. 5B

```
  1 MEDIQPTVELKSTEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANED 50
    ::: |.  ::.:.|..|:.....::  | .:| |.::....:  |..|..
 MDVDEGQDMSQVSGKESPPVSDTPDEG..DEPMPVPEDLSTTSG..AQQNSK 48

 51 EDAGEDSHKVKDEYSDRDENIHKPEPHGDAEESEMPYSYAREYSDYESIK 100
    .| | .| .|| |  . :|| . .|  |:. ..::.   |.: .  :| :
 49 SDRGMAS.NVKVETQSDEENGRACEMNGEECAEDLRMLDASGEKMNGSHR 97

101 LERHVPY...DNSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQC 147
     :   :.   :. | ..||:.|||:|||: ||: ||||||||||||||||
 98 DQGSSALSGVGGIRLPNGKLKCDICGIVCIGPNVLMVHKRSHTGERPFQC 147

148 NQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSV 197
     ||||||||||||||||||||.|||||||||||||||.|||||||||||||
148 NQCGASFTQKGNLLRHIKLHSGEKPFKCHLCNYACRRRDALTGHLRTHSV 197

198 EKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNPDLGDAASV.........E 239
    :||.|||::|||||||||||||||||:.:|:. :|.:...|         |
198 GKPHKCGYCGRSYKQRSSLEEHKERCHNYLESMGLPGVCPVIKEETNHNE 247

240 ARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCFDANYNPGY 289
      . ..:|.||.|||||||||||||||||||:|:|  |:..  .:
248 MAEDLCKIGAERSLVLDRLASNVAKRKSSMPQKFLGDK..CLSDMPYDSA 295

290 MYEKENEMMQTRMMDQAINNAISYLGAEAFAPLVQTPPAPTSEMVPVISS 339
     |||| :|| .:::||||||||.|||||.:|||||||:. ||:||||||
296 NYEKE.DMMTSHVMDQAINNAINYLGAESLAPLVQTPPGS.SEVVPVISS 343

340 VYPIALTRADMPM....GAPQEMEKKRILLPEKILPSERGLSPNNSAQDS 385
    :|.:  ...| |     :|.:.::.  :| ..| :.|||: ||.||.|||
344 MYQLHKPPSDGPPRSNHSAQDRVDNLLLLSKAKSVSSEREASPSNSCQDS 393

386 TDTDSN.HEDRQHLYQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLR 434
    |||:|| .|:|  |.  .: : |:||||:: ||| .|.:|:|:::.   .
394 TDTESNAEEQRSGLIYLTNHINPHARNGLA.LKEEQRAYEVLRAASENSQ 442

435 DSIKVINKEGEVMDVFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCG 481
    |.::|:...|| :.|::|:|||:|||||.||:||||||||||||||||||
443 DAFRVVSTSGEQLKVYKCEHCRVLFLDHVMYTIHMGCHGFRDPFECNMCG 492

482 YRSHDRYEFSSHIARGEHRAMLK 507
    |:|:||||||||.||||| |.
493 YHSQDRYEFSSHITRGEHRYHLS 518
```

FIG. 6

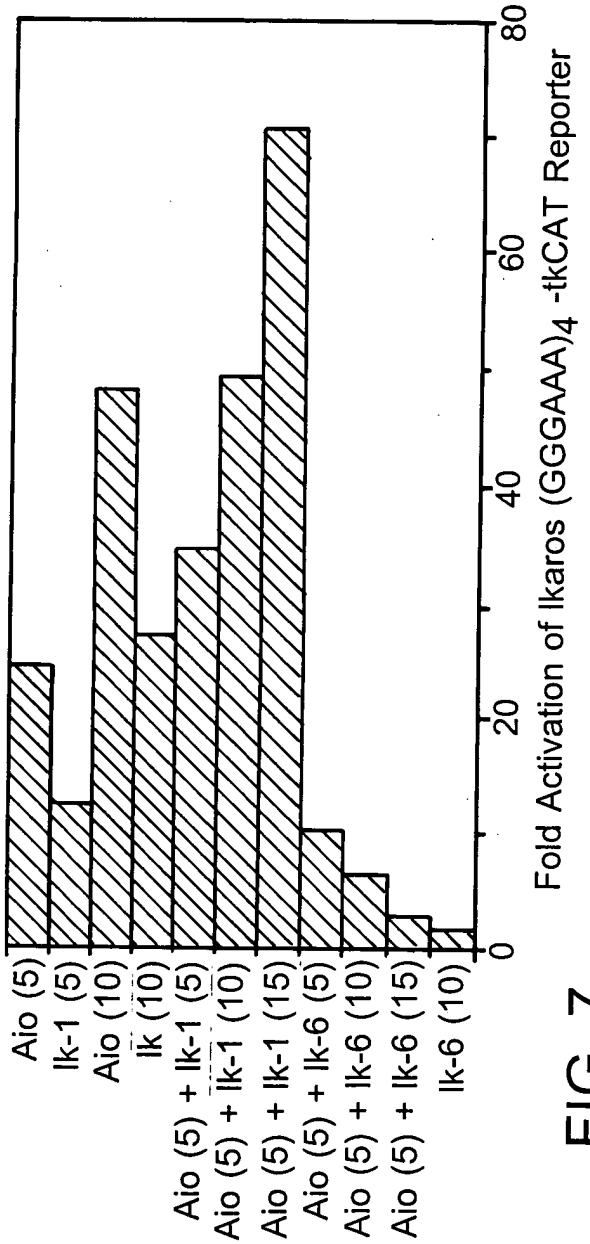


FIG. 7

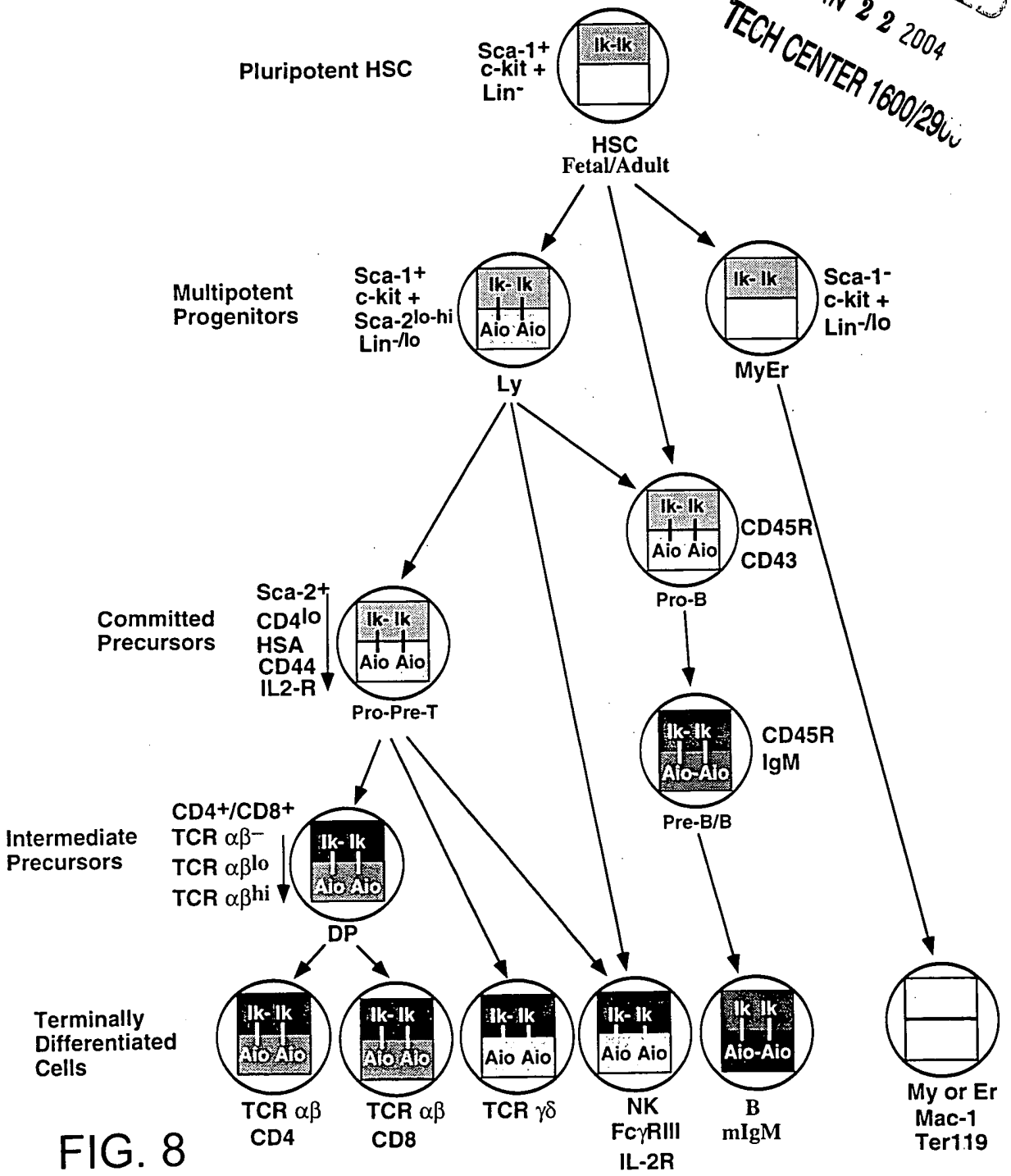


FIG. 8

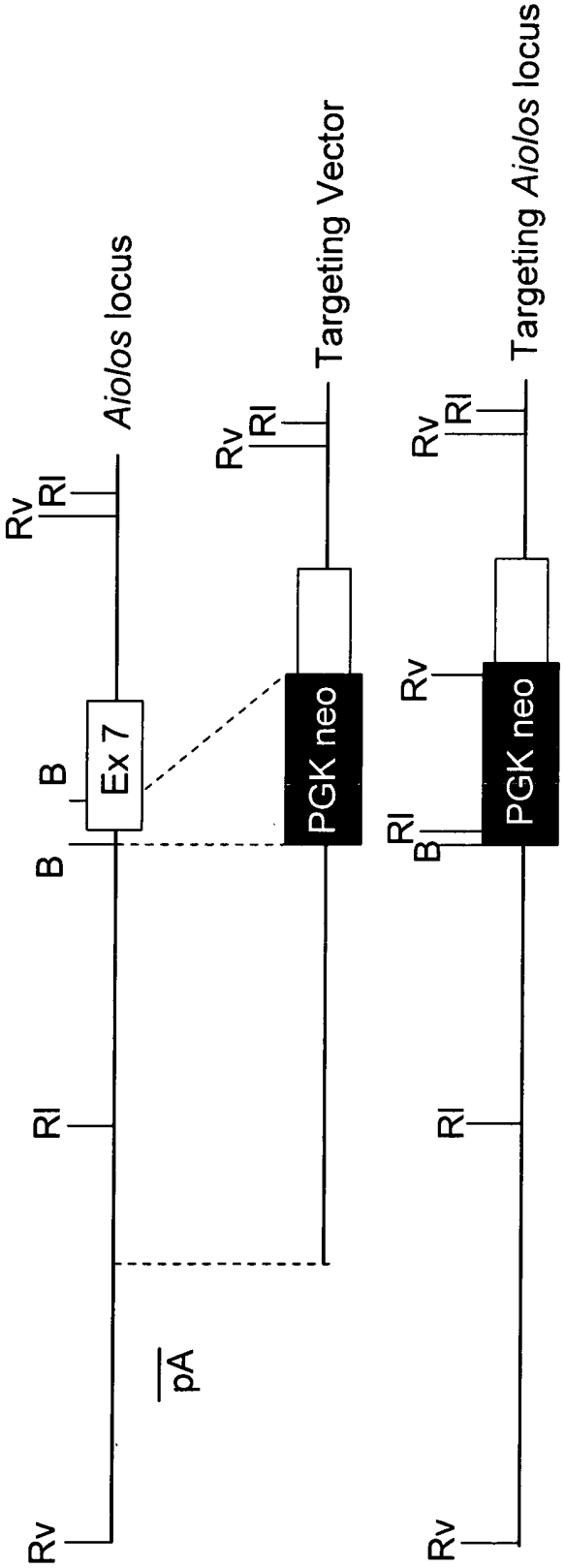


FIG. 9